

On page 25, line 22, change "Second" to -- Second, referring to figure 3C -- .

IN THE CLAIMS:

Please cancel Claims 1-15.

Please add the following claims.

16. A method for automatically analyzing nucleic acid data comprised of the steps:

- (a) performing an operation on a nucleic acid molecule;
- (b) generating data from the operation;
- (c) representing the data as an electrical signal;
- (d) operating on the electrical signal with a computing device to identify a subsignal corresponding to the operation; and

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(e) automatically analyzing the subsignal using a computing device to characterize a physical property of a nucleic acid component of the experiment.

17. A method as described in Claim 16 wherein the performing step (a) includes a polymerase chain reaction (PCR).

18. A method as described in Claim 17 wherein the performing step (a) includes PCR primers that are related to a genetic marker.

19. A method as described in Claim 18 wherein the genetic marker is polymorphic.

20. A method as described in Claim 19 wherein the automatic analyzing step (e) includes characterizing a size property of the nucleic acid component.

21. A method as described in Claim 20 wherein the genetic marker is a short tandem repeat.

22. A method as described in Claim 17 wherein the PCR products are labeled.

23. A method as described in Claim 22 wherein the generating step (b) includes detecting the label.

24. A method as described in Claim 16 wherein the generating step (b) includes recording the electrical signal in the memory of a computer.

25. A method as described in Claim 22 wherein the representing step (c) includes recording the electrical signal as a label intensity relative to a time or space coordinate.

26. A method as described in Claim 16 wherein the operating step (d) includes locating the data in the subsignal within a prespecified nucleic acid size range.

27. A method as described in Claim 16 wherein the analyzing step (e) includes characterizing a physical property corresponding to a molecular weight, nucleic acid size, nucleic acid quantity, nucleic acid concentration, or genome location.

28. A method as described in Claim 16 wherein the physical property of the nucleic acid component is used to positionally clone a gene.

29. A method as described in Claim 16 wherein the physical property of the nucleic acid component is used to genetically fingerprint an individual.

30. A system for automatically analyzing nucleic acid data comprising:

(a) means for performing an operation on a nucleic acid molecule;

(b) means for generating data from the operation;

(c) means for representing the data as an electrical signal;

(d) means for operating on the electrical signal with a computing device to identify a subsignal corresponding to the operation; and

(e) means for automatically analyzing the subsignal using a computing device to characterize a physical property of a nucleic acid component of the experiment.

31. A system as described in Claim 30 wherein the operation is an experiment.

32. A method for automatically analyzing nucleic acid material of an organism comprised of the steps:

- (a) obtaining nucleic acid material from the organism;
- (b) amplifying a location of the material that includes a polymorphic region;
- (c) determining a size property of the amplified location; and
- (d) automatically producing a genotype related to the size property of the amplified location of the nucleic acid material in an electronic acquisition system comprising a region having a radius of less than five feet at a rate exceeding 100 genotypes per hour.

33. A method as described in Claim 16 wherein the analyzing step (e) includes the step of exploiting a pattern in the data.